GenCore version 4.5
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OM protein - protein search, using sw model

Run on: March 1, 2001, 15:52:42 ; Search time 170.72 Seconds
                 (without alignments)
                 18.693 Million cell updates/sec

Title: US-09-331-631A-8_COPY_33_79
Perfect score: 275
Sequence: 1 GDDDPPKRYEDCRRRCEWDT..........QCEESCKSQYGEKDQQQRHR 47

Scoring table: BLOSUM62
                 Gapop 10.0 , Gapext 0.5

Database :   PIR_66:*
                 1: pir1:*
                 2: pir2:*
                 3: pir3:*
                 4: pir4:*

Searched: 195891 seqs, 67900655 residues

Total number of hits satisfying chosen parameters: 195891

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	275	100.0	588	1	FWCNAB	alpha-globulin B p
2	140	50.9	605	2	S06398	alpha-globulin typ
3	124	45.1	566	2	S22477	viclin precursor
4	94.5	34.4	509	2	S58059	alpha-globulin typ
5	90	32.7	810	2	T44430	protein PV100 (imp
6	75	27.3	47	2	JC5557	arginine/glutamate
7	67.5	24.5	471	2	A35480	variant surface gl
8	65.5	23.8	411	2	T29475	hypothetical prote
9	62	22.5	360	2	S50830	Machado-Joseph dis
10	61	22.2	189	2	F64533	co-chaperone and h
11	61	22.2	265	2	A33513	hypothetical prote
12	61	22.2	1905	2	T18267	multidrug resistan
13	60.5	22.0	897	2	T21688	hypothetical prote
14	60.5	22.0	1819	2	A71928	cag island protein
15	60	21.8	241	2	H81536	hypothetical prote
16	60	21.8	456	2	B72130	frame-shift with c
17	60	21.8	774	2	H81540	hypothetical prote
18	60	21.8	811	2	E72003	hypothetical prote
19	60	21.8	1927	2	G64585	cag pathogenicity
20	59.5	21.6	122	2	C53234	globulin-10 - maiz
21	59.5	21.6	230	2	C72256	rnfB-related prote
22	59.5	21.6	407	2	T02258	globulin1 - maize
23	59.5	21.6	540	2	S21825	viclin-like stora
24	59.5	21.6	573	2	A53234	globulin-1S, GLB1S
25	59.5	21.6	582	2	B53234	viclin-like stora
26	59.5	21.6	929	2	S75098	viclin-like stora
27	59.5	21.6	1234	2	T30100	hypothetical prote
28	59	21.5	85	2	E42825	Kruppel-type zinc
29	59	21.5	491	2	S52920	disintegrin (EC 3.
30	59	21.5	544	2	S52477	disintegrin (EC 3.
31	59	21.5	748	2	S66129	disintegrin (EC 3.
32	59	21.5	1339	1	S20052	DNA-directed DNA p
33	59	21.5	2150	2	S71629	sensory transducti
34	59	21.5	2165	2	T21371	hypothetical prote
35	58.5	21.3	1085	2	S62516	hypothetical colle
36	58	21.1	338	2	S04321	legumin B (clone P
37	57.5	20.9	419	2	T18450	hypothetical prote
38	57.5	20.9	225	2	B35387	rifin PFB0040c - m
39	57	20.7	342	2	F64210	brain-specific mem
40	57	20.7	527	2	B71625	hypothetical prote
41	57	20.7	330	2	JC7110	hypothetical prote
42	57	20.7	493	2	T01495	hypothetical prote
43	57	20.7	942	2	T02446	trichohyalin - hum
44	57	20.7	1898	1	A45973	trichohyalin - hum
45	56.5	20.5	388	2	T31887	hypothetical prote

ALIGNMENTS

RESULT 1
FWCNAB
alpha-globulin B precursor (clone C72) - upland cotton
N;Alternate names: seed storage protein; viclin precursor
C;Species: Gossypium hirsutum (upland cotton)
C;Date: 30-Sep-1991 #sequence_revision 30-Sep-1991 #text_change 16-Jul-1999
C;Accession: A30838; S06911
R;Chlan, C.A.; Pyle, J.B.; Legocki, A.B.; Dure III, L.
Plant Mol. Biol. 7, 475-489, 1986
A;Title: Developmental biochemistry of cottonseed embryogenesis and germination XVIII
A;Reference number: A30838
A;Accession: A30838
A;Molecule type: mRNA
A;Residues: 1-588 <CHL>
A;Cross-references: GB:M16891; NID:g167374; PIDN:AAA33071.1; PID:g167375
A;Experimental source: var. Coker 201
R;Chlan, C.A.; Boroto, K.; Kamalay, J.A.; Dure III, L.
Plant Mol. Biol. 9, 533-546, 1987
A;Title: Developmental biochemistry of cottonseed embryogenesis and germination XIX.
A;Accession: S06911
A;Reference number: S06911
A;Status: not compared with conceptual translation
A;Molecule type: DNA
A;Residues: 1-81 <CH2>
C;Comment: This is a seed storage protein.
C;Superfamily: glycinin
C;Keywords: glycoprotein; seed; storage protein
F;1-25/Domain: signal sequence #status predicted <SIG>
F;26-588/Product: alpha-globulin storage proprotein #status predicted <MAT>
F;417/Binding site: carbohydrate (Asn) (covalent) #status predicted

Qy   1 GDDDPPKRYEDCRRRCEWDTRGKEQQQCEESCKSQYGEKDQQQRHR 47
              ||||||||||||||||||||||||||||||||||||||||||||||
Db   33 GDDDPPKRYEDCRRRCEWDTRGKEQQQCEESCKSQYGEKDQQQRHR 79

Query Match   100.0%; Score 275; DB 1; Length 588;
Best Local Similarity   100.0%;
Matches   47; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 2
S06398
alpha-globulin type A precursor - upland cotton
N;Alternate names: seed storage protein
C;Species: Gossypium hirsutum (upland cotton)
C;Date: 31-Mar-1990 #sequence_revision 31-Mar-1990 #text_change 30-Sep-1993
C;Accession: S06398
R;Chlan, C.A.; Boroto, K.; Kamalay, J.A.; Dure III, L.
Plant Mol. Biol. 9, 533-546, 1987
A;Title: Developmental biochemistry of cottonseed embryogenesis and germination XIX.
A;Reference number: S06398

A;Accession: S06398
A;Status: not compared with conceptual translation
A;Molecule type:DNA
A;Residues: 1-605 <CHL>
A;Superfamily: glycinin
F;1-24/Domain: signal sequence #status predicted <SIG>
F;25-605/Product: alpha-globulin type A #status predicted <MAT>

Qy   Query Match   50.9%;   Score 140;   DB 2;   Length 605;
        Best Local Similarity   54.5%;   Pred. No. 5; 8e-08;
        Matches   24;   Conservative   11;   Mismatches   7;   Indels   2;   Gaps   1;

```
Qy    2 DDDPPKRYEDCRRRCEWDTRGQKEQOOCEESCKSQYGEKDQOQR 45
        :||| :||||||||:||: :|||||| ||: ::||| |  :|||
Db   34 EDDPQORYEDCRKRCQQLETRGQTEQDKCEDRSETQL--KEEQQR 75
```

RESULT 3
S22477
vicilin precursor - cacao
C;Species: Theobroma cacao (cacao)
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 17-Mar-1999
C;Accession: S22477; S22478; S18105; S22050
R;McHenry, L.; Fritz, P.J.
Plant Mol. Biol. 18, 1173-1176, 1992
A;Title: Comparison of the structure and nucleotide sequence of vicilin genes of cocoa a
A;Reference number: S22477; MUID:9288309
A;Accession: S22477
A;Molecule type: DNA
A;Residues: 1-566 <MCH>
A;Cross-references: EMBL:X62625
A;Accession: S22478
A;Molecule type: mRNA
A;Residues: 1-452 <MC2>
A;Genetics:
C;Cross-references: EMBL:X62626
A;Introns: 211/1; 269/3; 296/3; 391/3; 502/1
C;Superfamily: glycinin
C;Keywords: seed; storage protein
F;1-24/Domain: signal sequence #status predicted <SIG>
F;25-566/Product: vicilin #status predicted <MAT>

Query Match   45.1%;   Score 124;   DB 2;   Length 566;
Best Local Similarity   46.3%;   Pred. No. 3e-06;
Matches   19;   Conservative   12;   Mismatches   10;   Indels   0;   Gaps   0;

```
Qy    4 DPPKRYEDCRRRCEWDTRGQKEQOOCEESCKSQYGEKDQOQ 44
        || :||||| |:||: : :||:||:||:||:|: :||:||
Db   37 DPRQYEQCQORCESEATEREQEOCEQRCEREYKEQORQQ 77
```

RESULT 4
S08059
alpha-globulin type B precursor (tandem 1) - upland cotton (fragment)
N;Alternate names: seed storage protein
A;Reference number: S06398
C;Species: Gossypium hirsutum (upland cotton)
C;Date: 31-Mar-1990 #sequence_revision 31-Mar-1990 #text_change 30-Sep-1993
C;Accession: S08059
R;Chlan, C.A.; Borroto, K.; Kamalay, J.A.; Dure III, L.
Plant Mol. Biol. 9, 533-546, 1987
A;Title: Developmental biochemistry of cottonseed embryogenesis and germination. XIX. Se
A;Status: not compared with conceptual translation
A;Molecule type: DNA
A;Residues: 1-509 <CHL>
A;Superfamily: glycinin

Query Match   34.4%;   Score 94.5;   DB 2;   Length 509;
Best Local Similarity   36.4%;   Pred. No. 0.0043;

Matches   16;   Conservative   14;   Mismatches   11;   Indels   3;   Gaps   2;

```
Qy    4 DPPKRYEDCRRRCEWDTRGQKEQOOCEESCKSQYGEKDQOQORHR 47
        || :||||:|: | :: ::|||:|::|::|: :|::|| | |||
Db    1 DPQORYEQCQQECR--CQOEERQQPOCQORCLKRF-EQEQOQSQR 41
```

RESULT 5
T44430
protein PV100 [imported] - winter squash
C;Species: Cucurbita maxima (winter squash)
C;Date: 21-Jan-2000 #sequence_revision 21-Jan-2000 #text_change 21-Jul-2000
C;Accession: T44430
R;Yamada, K.; Shimada, T.; Kondo, M.; Nishimura, M.; Hara-Nishimura, I.
J. Biol. Chem. 274, 2563-2570, 1999
A;Title: Multiple functional proteins are produced by cleaving Asn-Gln bonds of a sin
A;Reference number: Z222767; MUID:99107919
A;Accession: T44430
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-810 <YAM>
A;Cross-references: EMBL:AB019195; NID:g3808061; PIDN:BAA34056.1; PID:g3808062

Query Match   32.7%;   Score 90;   DB 2;   Length 810;
Best Local Similarity   39.5%;   Pred. No. 0.02;
Matches   15;   Conservative   10;   Mismatches   13;   Indels   0;   Gaps   0;

```
Qy    5 PPKRYEDCRRRCEWDTRGQKEQOOCEESCKSQYGEKDQ 42
        | || |||: ||: ::|::|:: ||: |: :|: :|
Db   74 PRAEYEVCRLRCQVAERGVEQQORCEQVCEEERLREREQ 111
```

RESULT 6
JC5557
arginine/glutamate-rich 6.5k polypeptide - smooth loofah
C;Species: Luffa cylindrica (smooth loofah)
C;Date: 02-Sep-1997 #sequence_revision 05-Sep-1997 #text_change 07-May-1999
C;Accession: JC5557
R;Kimura, M.; Park, S.S.; Sakai, R.; Yamasaki, N.; Funatsu, G.
Biosci. Biotechnol. Biochem. 61, 984-988, 1997
A;Title: Primary structure of 6.5k-arginine/glutamate-rich polypeptide from the seeds
A;Reference number: JC5557; MUID:9735743
A;Accession: JC5557
A;Molecule type: protein
A;Residues: 1-47 <KIM>
A;Experimental source: seed
C;Comment: This protein is a storage protein whi ? provides nitrogen and carbon reser
F;12-33,16-29/Disulfide bonds: #status predicted

Query Match   27.3%;   Score 75;   DB 2;   Length 47;
Best Local Similarity   32.4%;   Pred. No. 0.069;
Matches   12;   Conservative   10;   Mismatches   15;   Indels   0;   Gaps   0;

```
Qy    5 PPKRYEDCRRRCEWDTRGQKEQOOCEESCKSQYGEKD 41
        | |||:||: |:||: |:|: :: :| |:
Db    5 PRTEYEACRVRCQVAEHGVEROQRRCOQVCEKRLRERE 41
```

RESULT 7
A35480
variant surface glycoprotein WRATatA precursor - Trypanosoma brucei rhodesiense
C;Species: Trypanosoma brucei rhodesiense
C;Date: 14-Sep-1990 #sequence_revision 14-Sep-1990 #text_change 26-Aug-1999
C;Accession: A35480
R;Reddy, L.V.; Hall, T.; Donelson, J.E.
Biochem. Biophys. Res. Commun. 169, 730-736, 1990
A;Title: Sequences of three VSG mRNAs expressed in a mixed population of Trypanosoma
A;Reference number: A35480; MUID:90290520
A;Accession: A35480
A;Status: preliminary
A;Molecule type: mRNA

RESULT 8
T29475
hypothetical protein T01D1.6 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 21-Jan-2000
C;Accession: T29475
R;Bradshaw, H.; Wohldmann, P.
submitted to the EMBL Data Library, November 1996
A;Description: The sequence of C. elegans cosmid T01D1.
A;Reference number: 220623
A;Accession: T29475
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-411 <BRA>
A;Experimental source: strain Bristol N2; clone T01D1
A;Genetics:
C;Genetics:
A;Gene: CESP:T01D1.6
A;Map position: 2
A;Introns: 25/3; 304/3
C;Superfamily: gliadin
A;Cross-references: EMBL:U80455; PIDN:AAB37887.1; GSPDB:GN00020; CESP:T01D1.6

Query Match   23.8%;   Score 65.5;   DB 2;   Length 411;
Best Local Similarity   35.9%;   Pred. No. 5;
Matches 14;   Conservative 11;   Mismatches 11;   Indels 3;   Gaps 2;

Qy   10 EDCRRRCEWDTRGQKE-QQQCEESCKS--QYGEKDQQQR 45
              ::||| .||:|||: ::|||:|||: :|::||||
Db   147 QDCQAACPQQQQPQQQCQQQCQQTTCQSDDQYSQQLIQQQ 185

RESULT 9
S50830
Machado-Joseph disease MJD1a protein - human
C;Species: Homo sapiens (man)
C;Date: 14-Jul-1995 #sequence_revision 21-Jul-1995 #text_change 28-May-1999
C;Accession: S50830
R;Kawaguchi, Y.; Okamoto, T.; Taniwaki, M.; Aizawa, M.; Inoue, M.; Katayama, S.; Kawakam
Nature Genet. 8, 221-228, 1994
A;Title: CAG expansions in a novel gene for Machado-Joseph disease at chromosome 14q32.1
A;Reference number: S50830; MUID:95179166
A;Accession: S50830
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-360 <KAW>
A;Cross-references: GB:S75513; NID:g833927; PIDN:AAB33571.1; PID:g833928

Query Match   22.5%;   Score 62;   DB 2;   Length 360;
Best Local Similarity   35.0%;   Pred. No. 11;
Matches 14;   Conservative 12;   Mismatches 12;   Indels 2;   Gaps 1;

Qy   10 EDCRRRCE--WDTRGQKEQQQCEESCKSQYGEKDQQQRHR 47
              ::|:| :||:::|||:::|:::|:::::||||||||:
Db   279 EELRKRREAYFEKQQQKKQQQKKQQQKKQQQQQQQQQQQR 318

RESULT 10
F64533
co-chaperone and heat shock protein - Helicobacter pylori (strain 26695)
C;Species: Helicobacter pylori
C;Date: 09-Aug-1997 #sequence_revision 09-Aug-1997 #text_change 08-Oct-1999
C;Accession: F64533
R;Tomb, J.F.; White, O.; Kerlavage, A.R.; Clayton, R.A.; Sutton, G.G.; Fleischmann, R
Peterson, S.; Loftus, B.; Richardson, D.; Dodson, R.; Khalak, H.G.; Glodek, A.; McKe
son, J.D.; Kelley, J.M.; Cotton, M.D.; Weidman, J.M.; Fujii, C.; Bowman, C.; Watthey,
Nature 388, 539-547, 1997
A;Authors: Wallin, E.; Hayes, W.S.; Borodovsky, M.; Karpk, P.D.; Smith, H.O.; Fraser,
A;Title: The complete genome sequence of the gastric pathogen Helicobacter pylori.
A;Reference number: A64520; MUID:97394467
A;Accession: F64533
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-189 <TOM>
A;Cross-references: GB:AE000532; GB:AE000511; NID:g2313184; PIDN:AAD07179.1; PID:g231
C;Superfamily: heat shock protein grpE

Query Match   22.2%;   Score 61;   DB 2;   Length 189;
Best Local Similarity   44.4%;   Pred. No. 7.8;
Matches 12;   Conservative 5;   Mismatches 10;   Indels 0;   Gaps 0;

Qy   17 EWDTRGQKEQQQCEESCKSQYGEKDQQ 43
              | ||| ||||:|| ::|||| |:|:
Db   8 EHDHLSQKEPEFCEKACKEQQYEEKQE 34

RESULT 11
A33513
hypothetical protein B - human T-cell lymphotropic virus type 1
C;Species: human T-cell lymphotropic virus type I, HTLV-1
C;Date: 20-Dec-1989 #sequence_revision 20-Dec-1989 #text_change 18-Jun-1993
C;Accession: A33513
R;Larocca, D.; Chao, L.A.; Seto, M.H.; Brunck, T.K.
Biochem. Biophys. Res. Commun. 163, 1006-1013, 1989
A;Title: Human T-cell leukemia virus minus strand transcription in infected T-cells.
A;Reference number: A33513; MUID:89391952
A;Accession: A33513
A;Status: preliminary; not compared with conceptual translation
A;Molecule type: genomic RNA
A;Residues: 1-265 <LAR>

Query Match   22.2%;   Score 61;   DB 2;   Length 265;
Best Local Similarity   26.5%;   Pred. No. 11;
Matches 13;   Conservative 17;   Mismatches 17;   Indels 2;   Gaps 1;

Qy   1 GDDDPPK--RYEDCRRCEWDTRGQKEQQQCEESCKSQYGEKDQQQRHR 47
             | ||:|| || ::|| :::||:|:::|||| ||:::||||::|||:
Db   123 GEKAPPRGETHRDRQRRAEEKRKRKKEREKEEEKQTAEYLKRKEEKAR 171

RESULT 12
T18267
multidrug resistance protein - slime mold (Dictyostelium discoideum)
C;Species: Dictyostelium discoideum
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
C;Accession: T18267
R;Shaulsky, G.; Kuspa, A.; Loomis, W.F.
submitted to the EMBL Data Library, January 1995
A;Description: An MDR transporter/serine protease gene is required for prestalk speci
A;Reference number: 218050
A;Accession: T18267
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-1905 <SHA>
A;Cross-references: EMBL:U20432; NID:g664839; PID:g664840; PIDN:AAA62212.1
C;Genetics:
A;Gene: tagB

A;Residues: 1-471 <RED>
A;Cross-references: GB:M33823; NID:g162487; PID:g162488
C;Superfamily: variant surface glycoprotein
C;Keywords: glycoprotein

Query Match   24.5%;   Score 67.5;   DB 2;   Length 471;
Best Local Similarity   31.0%;   Pred. No. 3.4;
Matches 13;   Conservative 11;   Mismatches 17;   Indels 1;   Gaps 1;

Qy   3 DDPPKRYEDCRRRCEWDTRGQKEQQQQCEESCKSQYGEKDQQ 44
             :| || |:::|| |:|||:||:::||:||:|:| ::
Db   402 NDKAKETE-CNSPCKWDKEEKDEKKRCKLSEEGKQAEKENQE 442

Qy   3 DDPPKRYEDCRRRCEWDTRGQKEQQQQCEESCKSQYGEKDQQ 44

Query Match   22.2%;   Score 61;   DB 2;   Length 1905;
Best Local Similarity   28.3%;   Pred. No. 60;
Matches   13;   Conservative   13;   Mismatches   20;   Indels   0;   Gaps   0;

Qy   2 DDDDPPKRYEDCRRRCEWDTRGQKEQQCEESCKSQYGEKDQQQRHR 47
          |:|| || | | | | |||:|:| ||||||:||||||
Db 1805 DQPPPPPQEQOQEOQOOQOQOOOEOOOOOOOOOOOOOEOOOOOOOOOQ 1850

RESULT 13
T21688
hypothetical protein F33A8.1 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
C;Accession: T21688
R;Matthews, L.
submitted to the EMBL Data Library, November 1996
A;Reference number: Z19459
A;Accession: T21688
A;Status: preliminary; translated from GB7/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-897 <WI>
A;Cross-references: EMBL:Z81525; PIDN:CAB04256.1; GSPDB:GN00020; CESP:F33A8.1
A;Experimental source: clone F33A8
C;Genetics:
A;Gene: CESP:F33A8.1
A;Map position: 2
A;Introns: 29/3; 56/3; 98/2; 225/2; 384/3; 419/1; 488/2; 517/3; 637/2

Query Match   22.0%;   Score 60.5;   DB 2;   Length 897;
Best Local Similarity   31.1%;   Pred. No. 35;
Matches   14;   Conservative   15;   Mismatches   15;   Indels   1;   Gaps   1;

Qy   3 DDPPKRYEDCRRRCEWDTRGQKEQQCEESCKSQYGEKDQQQRHR 47
          |:|| ||| || || ||:|:|:|:|||:|| |:|:|:| ||
Db 797 DDRKDRSKD-RRRQDSDEDKRGRERREDSGERRRGDRDRDRNK 840

RESULT 14
A71928
cag island protein - Helicobacter pylori (strain J99)
C;Species: Helicobacter pylori
A;Variety: strain J99
C;Date: 12-Feb-1999 #sequence_revision 12-Feb-1999 #text_change 08-Oct-1999
C;Accession: A71928
R;Alm, R.A.; Ling, L.S.L.; Moir, D.T.; King, B.L.; Brown, E.D.; Doig, P.C.; Smith, D.R.;
; Ives, C.; Gibson, R.; Merberg, D.; Mills, S.D.; Jiang, Q.; Taylor, D.E.; Vovis, G.F.;
Nature 397, 176-180, 1999
A;Reference number: A71928
A;Accession: A71928
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-1819 <ARN>
A;Cross-references: GB:AE001481; GB:AE001439; NID:g4155005; PIDN:AAD06047.1; PID:g415500
A;Experimental source: strain J99
C;Genetics:
A;Gene: orf13/14

Query Match   22.0%;   Score 60.5;   DB 2;   Length 1819;
Best Local Similarity   34.1%;   Pred. No. 65;
Matches   15;   Conservative   9;   Mismatches   13;   Indels   7;   Gaps   2;

Qy   7 KRYEDCRRRCEWDTRGQKEQQCEESCKSQ---YGEKDQQQRHR 47
          ||:|:|:||| | |||: |:||| |||| || |:||:|
Db 1242 KAYLDCVSR----ARNEKEKOECEKLLTPEARKFLEKRQQKDK 1281

RESULT 15
H81536

hypothetical protein CP0796 [imported] - Chlamydophila pneumoniae (strain AR39)
C;Species: Chlamydophila pneumoniae, Chlamydia pneumoniae
C;Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 18-Aug-2000
C;Accession: H81536
R;Read, T.D.; Brunham, R.C.; Shen, C.; Gill, S.R.; Heidelberg, J.F.; White, O.; Hicke
, C.; Dodson, R.; Gwinn, M.; Nelson, W.; DeBoy, R.; Kolonay, J.; McClarty, G.; Salzbe
Nucleic Acids Res. 28, 1397-1406, 2000
A;Title: Genome sequences of Chlamydia trachomatis MoPn and Chlamydia pneumoniae AR39
A;Reference number: A81500; MUID:20150255
submitted to the EMBL Data Library, November 1996
A;Accession: H81536; MUID:20150255
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-241 <REA>
A;Cross-references: GB:AE002239; GB:AE002161; NID:g7189708; PIDN:AAF38595.1; PID:g7189
A;Experimental source: strain AR39, HL cells
C;Genetics:
A;Gene: CP0796
C;Superfamily: Chlamydophila pneumoniae hypothetical protein CP0796

Query Match   21.8%;   Score 60;   DB 2;   Length 241;
Best Local Similarity   26.2%;   Pred. No. 12;
Matches   11;   Conservative   12;   Mismatches   19;   Indels   0;   Gaps   0;

Qy   2 DDDDPPKRYEDCRRRCEWDTRGQKEQQCEESCKSQYGEKDQQQ 43
          |:|| ||||| |:|| | | ||| |:|: :|| |:|
Db   51 DEDLRRAYTECQKRFQGDSGLESSEVRACREQLRERIQEFETQ 92

Search completed: March 1, 2001, 15:52:44
Job time: 568 sec